

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/908,453DATE: 10/16/98
TIME: 14:44:24

INPUT SET: S29199.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

1
2
3 (1) General Information
4
5 (i) APPLICANT: Ruvkun, Gary
6 Morris, Jason
7 Tissenbaum, Heidi
8
9 (ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED
10 MOLECULES AND METHODS
11
12 (iii) NUMBER OF SEQUENCES: 14
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Clark & Elbing LLP
16 (B) STREET: 176 Federal Street
17 (C) CITY: Boston
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 02110
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US97/13914
30 (B) FILING DATE: 07-AUG-1997
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 60/023,382
35 (B) FILING DATE: 07-AUG-1996
36
37
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Elbing, Karen L
41 (B) REGISTRATION NUMBER: 35,238
42 (C) REFERENCE/DOCKET NUMBER: 08472/704WO2
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 617-428-0200
46 (B) TELEFAX: 617-428-7045

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47 (C) TELEX:

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1146 amino acids

54 (B) TYPE: amino acid

55 (C) STRANDEDNESS: unknown

56 (D) TOPOLOGY: linear

57

58 (ii) MOLECULE TYPE: protein

59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

61

62	Met	His	Val	Asn	Ile	Leu	His	Pro	Gln	Leu	Gln	Thr	Met	Val	Glu	Gln
63	1			5					10						15	
64	Trp	Gln	Met	Arg	Glu	Arg	Pro	Ser	Leu	Glu	Thr	Glu	Asn	Gly	Lys	Gly
65				20					25					30		
66	Ser	Leu	Leu	Leu	Glu	Asn	Glu	Gly	Val	Ala	Asp	Ile	Ile	Thr	Met	Cys
67			35					40					45			
68	Pro	Phe	Gly	Glu	Val	Ile	Ser	Val	Val	Phe	Pro	Trp	Phe	Leu	Ala	Asn
69		50					55				60					
70	Val	Arg	Thr	Ser	Leu	Glu	Ile	Lys	Leu	Ser	Asp	Phe	Lys	His	Gln	Leu
71		65				70					75				80	
72	Phe	Glu	Leu	Ile	Ala	Pro	Met	Lys	Trp	Gly	Thr	Tyr	Ser	Val	Lys	Pro
73				85						90					95	
74	Gln	Asp	Tyr	Val	Phe	Arg	Gln	Leu	Asn	Asn	Phe	Gly	Glu	Ile	Glu	Val
75			100						105					110		
76	Ile	Phe	Asn	Asp	Asp	Gln	Pro	Leu	Ser	Lys	Leu	Glu	Leu	His	Gly	Thr
77			115					120					125			
78	Phe	Pro	Met	Leu	Phe	Leu	Tyr	Gln	Pro	Asp	Gly	Ile	Asn	Arg	Asp	Lys
79		130					135					140				
80	Glu	Leu	Met	Ser	Asp	Ile	Ser	His	Cys	Leu	Gly	Tyr	Ser	Leu	Asp	Lys
81		145				150					155				160	
82	Leu	Glu	Glu	Ser	Leu	Asp	Glu	Glu	Leu	Arg	Gln	Phe	Arg	Ala	Ser	Leu
83				165						170					175	
84	Trp	Ala	Arg	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Arg	Gly	Leu	Glu	Gly	Thr
85			180						185					190		
86	Ser	His	Tyr	Ala	Phe	Pro	Glu	Glu	Gln	Tyr	Leu	Cys	Val	Gly	Glu	Ser
87		195					200					205				
88	Cys	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Val	Lys	Ala	Ala	Lys	Leu	Ser	Tyr
89		210					215				220					
90	Gln	Met	Phe	Trp	Arg	Lys	Arg	Lys	Ala	Glu	Ile	Asn	Gly	Val	Cys	Glu
91		225				230					235				240	
92	Lys	Met	Met	Lys	Ile	Gln	Ile	Glu	Phe	Asn	Pro	Asn	Glu	Thr	Pro	Lys
93				245						250					255	
94	Ser	Leu	Leu	His	Thr	Phe	Leu	Tyr	Glu	Met	Arg	Lys	Leu	Asp	Val	Tyr
95			260						265					270		
96	Asp	Thr	Asp	Asp	Pro	Ala	Asp	Glu	Gly	Trp	Phe	Leu	Gln	Leu	Ala	Gly
97		275						280					285			
98	Arg	Thr	Thr	Phe	Val	Thr	Asn	Pro	Asp	Val	Lys	Leu	Thr	Ser	Tyr	Asp
99		290					295					300				

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100	Gly	Val	Arg	Ser	Glu	Leu	Glu	Ser	Tyr	Arg	Cys	Pro	Gly	Phe	Val	Val
101	305					310					315					320
102	Arg	Arg	Gln	Ser	Leu	Val	Leu	Lys	Asp	Tyr	Cys	Arg	Pro	Lys	Pro	Leu
103					325					330					335	
104	Tyr	Glu	Pro	His	Tyr	Val	Arg	Ala	His	Glu	Arg	Lys	Leu	Ala	Leu	Asp
105				340					345					350		
106	Val	Leu	Ser	Val	Ser	Ile	Asp	Ser	Thr	Pro	Lys	Gln	Ser	Lys	Asn	Ser
107			355					360					365			
108	Asp	Met	Val	Met	Thr	Asp	Phe	Arg	Pro	Thr	Ala	Ser	Leu	Lys	Gln	Val
109	370						375					380				
110	Ser	Leu	Trp	Asp	Leu	Asp	Ala	Asn	Leu	Met	Ile	Arg	Pro	Val	Asn	Ile
111	385				390					395					400	
112	Ser	Gly	Phe	Asp	Phe	Pro	Ala	Asp	Val	Asp	Met	Tyr	Val	Arg	Ile	Glu
113				405					410						415	
114	Phe	Ser	Val	Tyr	Val	Gly	Thr	Leu	Thr	Leu	Ala	Ser	Lys	Ser	Thr	Thr
115			420					425					430			
116	Lys	Val	Asn	Ala	Gln	Phe	Ala	Lys	Trp	Asn	Lys	Glu	Met	Tyr	Thr	Phe
117			435					440					445			
118	Asp	Leu	Tyr	Met	Lys	Asp	Met	Pro	Pro	Ser	Ala	Val	Leu	Ser	Ile	Arg
119	450						455					460				
120	Val	Leu	Tyr	Gly	Lys	Val	Lys	Leu	Lys	Ser	Glu	Glu	Phe	Glu	Val	Gly
121	465				470					475					480	
122	Trp	Val	Asn	Met	Ser	Leu	Thr	Asp	Trp	Arg	Asp	Glu	Leu	Arg	Gln	Gly
123				485					490						495	
124	Gln	Phe	Leu	Phe	His	Leu	Trp	Ala	Pro	Glu	Pro	Thr	Ala	Asn	Arg	Ser
125			500					505					510			
126	Arg	Ile	Gly	Glu	Asn	Gly	Ala	Arg	Ile	Gly	Thr	Asn	Ala	Ala	Val	Thr
127		515					520					525				
128	Ile	Glu	Ile	Ser	Ser	Tyr	Gly	Gly	Arg	Val	Arg	Met	Pro	Ser	Gln	Gly
129	530						535					540				
130	Gln	Tyr	Thr	Tyr	Leu	Val	Lys	His	Arg	Ser	Thr	Trp	Thr	Glu	Thr	Leu
131	545				550						555				560	
132	Asn	Ile	Met	Gly	Asp	Asp	Tyr	Glu	Ser	Cys	Ile	Arg	Asp	Pro	Gly	Tyr
133				565					570					575		
134	Lys	Lys	Leu	Gln	Met	Leu	Val	Lys	Lys	His	Glu	Ser	Gly	Ile	Val	Leu
135			580					585					590			
136	Glu	Glu	Asp	Glu	Gln	Arg	His	Val	Trp	Met	Trp	Arg	Arg	Tyr	Ile	Gln
137			595				600					605				
138	Lys	Gln	Glu	Pro	Asp	Leu	Leu	Ile	Val	Leu	Ser	Glu	Leu	Ala	Phe	Val
139	610					615					620					
140	Trp	Thr	Asp	Arg	Glu	Asn	Phe	Ser	Glu	Leu	Tyr	Val	Met	Leu	Glu	Lys
141	625				630					635					640	
142	Trp	Lys	Pro	Pro	Ser	Val	Ala	Ala	Ala	Leu	Thr	Leu	Leu	Gly	Lys	Arg
143				645					650					655		
144	Cys	Thr	Asp	Arg	Val	Ile	Arg	Lys	Phe	Ala	Val	Glu	Lys	Leu	Asn	Glu
145			660					665					670			
146	Gln	Leu	Ser	Pro	Val	Thr	Phe	His	Leu	Phe	Ile	Leu	Pro	Leu	Ile	Gln
147		675					680					685				
148	Ala	Leu	Lys	Tyr	Glu	Pro	Arg	Ala	Gln	Ser	Glu	Val	Gly	Met	Met	Leu
149	690					695					700					
150	Leu	Thr	Arg	Ala	Leu	Cys	Asp	Tyr	Arg	Ile	Gly	His	Arg	Leu	Phe	Trp
151	705				710					715					720	
152	Leu	Leu	Arg	Ala	Glu	Ile	Ala	Arg	Leu	Arg	Asp	Cys	Asp	Leu	Lys	Ser

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153				725				730					735			
154	Glu	Glu	Tyr	Arg	Arg	Ile	Ser	Leu	Leu	Met	Glu	Ala	Tyr	Leu	Arg	Gly
155				740				745					750			
156	Asn	Glu	Glu	His	Ile	Lys	Ile	Ile	Thr	Arg	Gln	Val	Asp	Met	Val	Asp
157				755				760					765			
158	Glu	Leu	Thr	Arg	Ile	Ser	Thr	Leu	Val	Lys	Gly	Met	Pro	Lys	Asp	Val
159				770				775					780			
160	Ala	Thr	Met	Lys	Leu	Arg	Asp	Glu	Leu	Arg	Ser	Ile	Ser	His	Lys	Met
161				785				790					795			800
162	Glu	Asn	Met	Asp	Ser	Pro	Leu	Asp	Pro	Val	Tyr	Lys	Leu	Gly	Glu	Met
163					805					810						815
164	Ile	Ile	Asp	Lys	Ala	Ile	Val	Leu	Gly	Ser	Ala	Lys	Arg	Pro	Leu	Met
165				820					825							830
166	Leu	His	Trp	Lys	Asn	Lys	Asn	Pro	Lys	Ser	Asp	Leu	His	Leu	Pro	Phe
167				835				840					845			
168	Cys	Ala	Met	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu
169				850				855					860			
170	Val	Leu	Gln	Val	Leu	Glu	Val	Met	Asp	Asn	Ile	Trp	Lys	Ala	Ala	Asn
171						870				875						880
172	Ile	Asp	Cys	Cys	Leu	Asn	Pro	Tyr	Ala	Val	Leu	Pro	Met	Gly	Glu	Met
173					885					890						895
174	Ile	Gly	Ile	Ile	Glu	Val	Val	Pro	Asn	Cys	Lys	Thr	Ile	Phe	Glu	Ile
175				900					905							910
176	Gln	Val	Gly	Thr	Gly	Phe	Met	Asn	Thr	Ala	Val	Arg	Ser	Ile	Asp	Pro
177				915				920					925			
178	Ser	Phe	Met	Asn	Lys	Trp	Ile	Arg	Lys	Gln	Cys	Gly	Ile	Glu	Asp	Glu
179				930				935					940			
180	Lys	Lys	Lys	Ser	Lys	Lys	Asp	Ser	Thr	Lys	Asn	Pro	Ile	Glu	Lys	Lys
181						950				955						960
182	Ile	Asp	Asn	Thr	Gln	Ala	Met	Lys	Lys	Tyr	Phe	Glu	Ser	Val	Asp	Arg
183					965					970						975
184	Phe	Leu	Tyr	Ser	Cys	Val	Gly	Tyr	Ser	Val	Ala	Thr	Tyr	Ile	Met	Gly
185				980					985							990
186	Ile	Lys	Asp	Arg	His	Ser	Asp	Asn	Leu	Met	Leu	Thr	Glu	Asp	Gly	Lys
187				995				1000					1005			
188	Tyr	Val	His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	His	Gly	Lys	Thr	Lys
189				1010				1015					1020			
190	Leu	Gly	Ile	Gln	Arg	Asp	Arg	Gln	Pro	Phe	Ile	Leu	Thr	Glu	His	Phe
191						1030				1035						1040
192	Met	Thr	Val	Ile	Arg	Ser	Gly	Lys	Ser	Val	Asp	Gly	Asn	Ser	His	Glu
193					1045					1050						1055
194	Leu	Gln	Lys	Phe	Lys	Thr	Leu	Cys	Val	Glu	Ala	Tyr	Glu	Val	Met	Trp
195				1060					1065							1070
196	Asn	Asn	Arg	Asp	Leu	Phe	Val	Ser	Leu	Phe	Thr	Leu	Met	Leu	Gly	Met
197				1075				1080					1085			
198	Glu	Leu	Pro	Glu	Leu	Ser	Thr	Lys	Ala	Asp	Leu	Asp	His	Leu	Lys	Lys
199				1090				1095					1100			
200	Thr	Leu	Phe	Cys	Asn	Gly	Glu	Ser	Lys	Glu	Glu	Ala	Arg	Lys	Phe	Phe
201					1110					1115						1120
202	Ala	Gly	Ile	Tyr	Glu	Glu	Ala	Phe	Asn	Gly	Ser	Trp	Ser	Thr	Lys	Thr
203					1125					1130						1135
204	Asn	Trp	Leu	Phe	His	Ala	Val	Lys	His	Tyr						
205				1140					1145							

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206

207

(2) INFORMATION FOR SEQ ID NO:2:

208

209

(i) SEQUENCE CHARACTERISTICS:

210

(A) LENGTH: 3504 base pairs

211

(B) TYPE: nucleic acid

212

(C) STRANDEDNESS: double

213

(D) TOPOLOGY: linear

214

215

(ii) MOLECULE TYPE: cDNA

216

217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

218

219	CGGAAGCCAT	GGAGCTCGAG	ATCTGATTGC	TGGACACGGA	CGGAAC TCCG	ACGTATCTCG	60
220	CAGATGCATG	TTAACATTTT	ACATCCACAA	CTGCAAACGA	TGGTCGAGCA	GTGGCAAATG	120
221	CGAGAACGCC	CATCGCTGGA	GACCGAGAAT	GGCAAAGGAT	CGCTGCCTCT	GGAAAATGAA	180
222	GGTGTGCGCAG	ATATCATCAC	TATGTGTCCA	TTCGGAGAAG	TTATTAGTGT	AGTATTTCCG	240
223	TGGTTTCTTG	CAAAATGTGCG	AACATCGCTA	GAAATCAAGC	TATCAGATTT	CAACATCAA	300
224	CTTTTCGAAT	TGATTGCTCC	GATGAAGTGG	GGAACATATT	CCGTAAAGCC	ACAGGATTAT	360
225	GTGTTTCAGAC	AGTTGAATAA	TTTCGGCGAA	ATTGAAGTTA	TATTTAACGA	CGATCAACCC	420
226	CTGTCGAAAT	TAGAGCTCCA	CGGCACTTTC	CCAATGCTTT	TTCTCTACCA	ACCTGATGGA	480
227	ATAAACAGGG	ATAAAGAATT	AATGAGTGAT	ATAAGTCATT	GTCTAGGATA	CTCACTGGAT	540
228	AAACTGGAAG	AGAGCCTCGA	TGAGGAACTC	CGTCAATTTT	GTGCTTCTCT	CTGGGCTCGT	600
229	ACGAAGAAAA	CGTGCTTGAC	ACGTGGACTT	GAGGGTACCA	GTCACTACGC	GTTCCCGCAA	660
230	GAACAGTACT	TGTGTGTTGG	TGAATCGTGC	CCGAAAGATT	TGGAATCAAA	AGTCAAGGCT	720
231	GCCAAGCTGA	GTTATCAGAT	GTTTTGGAGA	AAACGTAAG	CGGAAATCAA	TGGAGTTTGC	780
232	GAGAAAATGA	TGAAGATTCA	AATTGAATTC	AATCCGAACG	AAACTCCGAA	ATCTCTGCTT	840
233	CACACGTTTC	TCTACGAAAT	GCGAAAATTG	GATGTATACG	ATACCGATGA	TCCCTGCAGAT	900
234	GAAGGATGGT	TTCTTCAATT	GGCTGGACGT	ACCACGTTTG	TTACAAAATCC	AGATGTCAAA	960
235	CTTACGTCTT	ATGATGGTGT	CCGTTCGGAA	CTGGAAAGCT	ATCGATGCCC	TGGATTCTGTT	1020
236	GTTCCGCCGAC	AATCACTAGT	CCTCAAAGAC	TATTGTGCGC	CAAAACCACT	CTACGAACCA	1080
237	CATTATGTGA	GAGCACACGA	ACGAAAACCT	GCTCTAGACG	TGCTCAGCGT	GTCTATAGAT	1140
238	AGCACACCAA	AACAGAGCAA	GAACAGTGAC	ATGGTTATGA	CTGATTTTTC	TCCGACAGCT	1200
239	TCACTCAAAC	AAGTTTCACT	TTGGGACCTT	GACGCGAATC	TTATGATACG	GCCTGTGAAT	1260
240	ATTTCTGGAT	TCCGATTTCC	GGCCGACGTG	GATATGTACG	TTCGAATCGA	ATTCAAGTGA	1320
241	TATGTGGGGA	CACTGACGCT	GGCATCAAAA	TCTACAACAA	AAGTGAATGC	TCAATTTGCA	1380
242	AAATGGAATA	AGGAAATGTA	CACTTTTGAT	CTATACATGA	AGGATATGCC	ACCATCTGCA	1440
243	GTACTCAGCA	TTCGTGTTTT	GTACGGAAAA	GTGAAATTAA	AAAGTGAAGA	ATTCTGAAGTT	1500
244	GGTTGGGTAA	ATATGTCCCT	AACCGATTGG	AGAGATGAAC	TACGACAAGG	ACAATTTTTA	1560
245	TTCCATCTGT	GGGCTCCTGA	ACCGACTGCC	AATCGTAGTA	GGATCGGAGA	AAATGGAGCA	1620
246	AGGATAGGCA	CCAACGCAGC	GGTTACAATT	GAAATCTCAA	GTTATGGTGG	TAGAGTTCGA	1680
247	ATGCCGAGTC	AAGGACAATA	CACATATCTC	GTCAAGCACC	GAAGTACTTG	GACGGAAACT	1740
248	TTGAATATTA	TGGGTGATGA	CTATGAGTCG	TGTATCAGAG	ATCCAGGATA	TAAGAAGCTT	1800
249	CAGATGCTTG	TCAAGAAGCA	TGAATCTGGA	ATTGTATTAG	AGGAAGATGA	ACAACGTCAT	1860
250	GTCTGGATGT	GGAGGAGATA	CATTCAAAAAG	CAGGAGCCTG	ATTTGCTCAT	TGTGCTCTCC	1920
251	GAAC TCGCAT	TTGTGTGGAC	TGATCGTGAG	AACTTTTCCG	AGCTCTATGT	GATGCTTGAA	1980
252	AAATGGA AAC	CGCCGAGTGT	GGCAGCCGCG	TTGACTTTGC	TTGGAAAACG	TTGCACGGAT	2040
253	CGTGTGATT C	GAAAGTTTGC	AGTGGAGAAG	TTGAATGAGC	AGCTGAGCCC	GGTCACATTC	2100
254	CATCTTTTCA	TATTGCCTCT	CATACAGGCG	TTGAAGTACG	AACCGCGTGC	TCAATCGGAA	2160
255	GTTGGAA TGA	TGCTCTTGAC	TAGAGCTCTC	TGCGATTATC	GAATTGGACA	TCGACTTTTC	2220
256	TGGCTGCTCC	GTGCAGAGAT	TGCTCGTTTG	AGAGATTGTG	ATCTGAAAAG	TGAAGAATAT	2280
257	CGCCGTATCT	CACTTCTGAT	GGAAGCTTAC	CTCCGTGGAA	ATGAAGAGCA	CATCAAGATC	2340
258	ATCACCCGAC	AAGTTGACAT	GGTTGATGAG	CTCACACGAA	TCAGCACTCT	TGTCAAAGGA	2400

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: US97/13914